

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2005, 12:05:14 ; Search time 1226.94 Seconds  
(without alignments)  
10910.664 Million cell updates/sec

Title: US-09-310-638-1

Perfect score: 2256  
Sequence: 1 CCTCTCTCCCTCATCTTTG.....AAAAAAAAAAAAAAAAAAAA 2256

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 5401638 seqs, 2966923429 residues

Total number of hits satisfying chosen parameters: 10803276

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications NA.\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1722	76.3	1725	9	US-09-810-861B-5
2	1719.6	76.2	5767	9	US-09-810-861B-3
3	1719.6	76.2	14446	9	US-09-810-861B-4
4	740	33.8	740	16	US-10-029-386-22811
5	594	26.3	594	16	US-10-029-386-25399
6	501	22.2	501	16	US-10-029-386-11696
7	421.4	18.7	2416	16	US-10-032-233-15
8	421.4	18.7	2416	16	US-10-032-233-19
9	421.4	18.7	2416	16	US-10-032-233-33
10	421.4	18.7	2416	18	US-10-413-432-15
11	421.4	18.7	2416	18	US-10-413-432-19

12	421.4	18.7	2416	18	US-10-413-432-33	Sequence 33, Appl1
13	421.4	18.7	2416	18	US-10-324-466-15	Sequence 15, Appl1
14	421.4	18.7	2416	18	US-10-324-466-19	Sequence 19, Appl1
15	421.4	18.7	2416	18	US-10-324-466-33	Sequence 33, Appl1
16	419.8	18.6	1725	17	US-10-326-892-1	Sequence 1, Appl1
17	419.8	18.6	1725	18	US-10-326-892-1	Sequence 1, Appl1
18	419.8	18.6	1967	9	US-09-748-739A-1	Sequence 1, Appl1
19	419.8	18.6	2416	9	US-09-748-739A-3	Sequence 3, Appl1
20	419.8	18.6	2416	16	US-10-032-233-11	Sequence 11, Appl1
21	419.8	18.6	2416	16	US-10-032-233-17	Sequence 17, Appl1
22	419.8	18.6	2416	16	US-10-032-233-27	Sequence 27, Appl1
23	419.8	18.6	2416	16	US-10-032-233-35	Sequence 35, Appl1
24	419.8	18.6	2416	18	US-10-413-432-11	Sequence 11, Appl1
25	419.8	18.6	2416	18	US-10-413-432-17	Sequence 17, Appl1
26	419.8	18.6	2416	18	US-10-413-432-27	Sequence 27, Appl1
27	419.8	18.6	2416	18	US-10-413-432-35	Sequence 35, Appl1
28	419.8	18.6	2416	18	US-10-324-466-11	Sequence 11, Appl1
29	419.8	18.6	2416	18	US-10-324-466-17	Sequence 17, Appl1
30	419.8	18.6	2416	18	US-10-324-466-27	Sequence 27, Appl1
31	419.8	18.6	2416	18	US-10-324-466-35	Sequence 35, Appl1
32	418.2	18.5	2381	9	US-09-880-107-2271	Sequence 5, Appl1
33	418.2	18.5	2416	9	US-09-748-739A-5	Sequence 5, Appl1
34	418.2	18.5	2416	9	US-09-748-739A-7	Sequence 7, Appl1
35	418.2	18.5	2416	9	US-09-748-739A-16	Sequence 16, Appl1
36	418.2	18.5	2416	16	US-10-032-233-13	Sequence 13, Appl1
37	418.2	18.5	2416	16	US-10-032-233-29	Sequence 29, Appl1
38	418.2	18.5	2416	16	US-10-032-233-31	Sequence 31, Appl1
39	418.2	18.5	2416	16	US-10-032-233-37	Sequence 37, Appl1
40	418.2	18.5	2416	16	US-10-032-233-39	Sequence 39, Appl1
41	418.2	18.5	2416	16	US-10-032-233-43	Sequence 43, Appl1
42	418.2	18.5	2416	18	US-10-413-432-13	Sequence 13, Appl1
43	418.2	18.5	2416	18	US-10-413-432-29	Sequence 29, Appl1
44	418.2	18.5	2416	18	US-10-413-432-31	Sequence 31, Appl1
45	418.2	18.5	2416	18	US-10-413-432-37	Sequence 37, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-810-861B-5  
Sequence 5, Application US/09810861B  
Patent No. US20020162140A1  
GENERAL INFORMATION:  
APPLICANT: Mor, Tsafira S.  
APPLICANT: Soreq, Hermona  
APPLICANT: Amltzen, Charles J.  
TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN  
FILE REFERENCE: BTI-45  
CURRENT APPLICATION NUMBER: US/09/810, 861B  
CURRENT FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/190,440  
PRIOR FILING DATE: 2000-03-17  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn Ver. 3.1  
SEQ ID NO 5  
LENGTH: 1725  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
OTHER INFORMATION: human acetylcholinesterase gene optimized for  
OTHER INFORMATION: expression in plants  
US-09-810-861B-5

Query Match 76.3%; Score 1722; DB 9; Length 1725;  
Best local Similarity 100.0%; Pred. No. 0;  
Matches 1722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
160 ATGAGGCGCCGCGAGTGTCTGCTGACACGCTTCCCTGCTCCACCTCTCTCTC 219

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2005, 06:55:38 ; Search time 364.497 Seconds  
(without alignments)  
10127.488 Million cell updates/sec

Title: US-09-310-638-1

Perfect score: 2256  
Sequence: 1 CCTCTCTCCCTCATCTTTG.....AAAAAAAAAAAAAAAAAAAA 2256

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/prodata/1/ina/5A COMB.seq: \*  
2: /cgn2\_6/prodata/1/ina/5B COMB.seq: \*  
3: /cgn2\_6/prodata/1/ina/6A COMB.seq: \*  
4: /cgn2\_6/prodata/1/ina/6B COMB.seq: \*  
5: /cgn2\_6/prodata/1/ina/PCUS COMB.seq: \*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2256	100.0	2256	2 US-08-318-826A-5	Sequence 5, Appli
2	2256	100.0	2256	2 US-08-370-156-1	Sequence 1, Appli
3	2256	100.0	2256	3 US-08-814-095-1	Sequence 1, Appli
4	2023.2	89.7	2158	4 US-09-949-016-1192	Sequence 1192, Ap
5	2023.2	89.7	2158	4 US-09-949-016-1193	Sequence 1193, Ap
6	1888	83.7	3096	2 US-08-318-826A-6	Sequence 6, Appli
7	1888	83.7	3096	2 US-08-370-156-3	Sequence 3, Appli
8	1888	83.5	3096	2 US-08-814-095-3	Sequence 3, Appli
9	1883.8	83.5	3016	2 US-08-318-826A-7	Sequence 7, Appli
10	1883.8	83.5	3016	2 US-08-370-156-5	Sequence 5, Appli
11	1883.8	83.5	3016	2 US-08-814-095-5	Sequence 5, Appli
12	1845	81.8	1845	3 US-07-732-962A-1	Sequence 1, Appli
13	1845	81.8	1845	5 PCT-US92-06106-1	Sequence 1, Appli
14	1722	76.3	1725	4 US-09-810-861B-5	Sequence 5, Appli
15	1719.6	76.2	1446	4 US-09-810-861B-3	Sequence 3, Appli
16	1719.6	76.2	1446	4 US-09-810-861B-4	Sequence 4, Appli
17	1357	60.2	9885	4 US-09-949-016-12934	Sequence 12934, A
18	1357	60.2	9885	4 US-09-949-016-12935	Sequence 12935, A
19	1357	60.2	35060	3 US-08-814-095-7	Sequence 7, Appli
20	418.2	18.5	2381	2 US-08-318-826A-9	Sequence 9, Appli
21	418.2	18.5	2416	2 US-08-318-826A-8	Sequence 8, Appli
22	418.2	18.5	2416	4 US-09-334-489-1	Sequence 1, Appli
23	418.2	18.5	2444	4 US-09-949-016-5275	Sequence 5275, Ap
24	416.6	18.5	2400	6 5215908-13	Patent No. 5215909
25	416.6	18.5	2400	6 5215909-13	Patent No. 5215909
26	416.6	18.5	2416	3 US-09-334-489-2	Sequence 2, Appli
27	376	16.7	1215	2 US-08-370-156-26	Sequence 26, Appli

28	374	16.6	374	2 US-08-370-156-24	Sequence 24, Appli
29	371.4	16.5	6867	4 US-09-949-016-17017	Sequence 17017, A
30	340.4	15.1	2445	6 5215909-9	Patent No. 5215909
31	340.4	15.1	2445	6 5215909-9	Patent No. 5215909
32	185.6	8.2	764	6 5215909-7	Patent No. 5215909
33	185.6	8.2	764	6 5215909-7	Patent No. 5215909
34	142.6	6.3	3018	1 US-08-347-718B-3	Sequence 3, Appli
35	142.6	6.3	3018	1 US-08-482-262-3	Sequence 3, Appli
36	141	6.2	2734	4 US-09-569-611C-5	Sequence 5, Appli
37	141	6.2	2781	4 US-09-569-611C-6	Sequence 6, Appli
38	141	6.2	3018	6 5200183-1	Patent No. 5200183
39	141	6.2	3018	6 5200183-1	Patent No. 5200183
40	139.4	6.2	1746	4 US-10-023-515-3	Sequence 3, Appli
41	139.4	6.2	2158	4 US-10-023-515-1	Sequence 1, Appli
42	139.4	6.2	2184	1 US-08-445-050-8	Sequence 8, Appli
43	139.4	6.2	2184	1 US-08-204-691-8	Sequence 8, Appli
44	139.4	6.2	2344	3 US-09-347-878-31	Sequence 31, Appli
45	139.4	6.2	2375	4 US-09-949-016-1976	Sequence 3976, Ap

## ALIGNMENTS

RESULT 1  
US-08-318-826A-5  
Sequence 5, Application US/08318826A

Patent No. 5891725

GENERAL INFORMATION:

APPLICANT: Soreq, Hermona

APPLICANT: Zakut, Haim

APPLICANT: Eckstein, Fritz

TITLE OF INVENTION: Synthetic Antisense

TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSER: Kohn & Associates

STREET: 30500 No. 5891725thwestern Hwy., Suite 410

CITY: Farmington Hills

STATE: Michigan

COUNTRY: US

ZIP: 48334

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/318,826A

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Kohn, Kenneth I.

REGISTRATION NUMBER: 30,955

REFERENCE/DOCKET NUMBER: 2391.00001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (248) 539-5050

TELEFAX: (248) 539-5055

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 2256 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

FEATURES:

OTHER INFORMATION: /note="Splice variant: Exons 1, 2,

OTHER INFORMATION: 3, 4 and 6"

US-08-318-826A-5

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

# OM nucleic - nucleic search, using sw model

Run on: March 3, 2005, 12:05:14 ; Search time 1683.78 Seconds  
(without alignments)  
10910.664 Million cell updates/sec

Title: US-09-310-638-3  
Perfect score: 3096  
Sequence: 1 CCTCTCCTCCCTCATCTTTG.....AAAAAAAAAAAAAAAAAAAA 3096

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 5401638 seqs, 2866923429 residues  
Total number of hits satisfying chosen parameters: 10803276

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1722.4	55.6	1725	US-09-810-861B-5	Sequence 5, Appl1
2	1720	55.6	5767	US-09-810-861B-3	Sequence 3, Appl1
3	1720	55.6	14446	US-09-810-861B-4	Sequence 4, Appl1
4	740	23.9	740	US-10-029-386-22811	Sequence 22811, A
5	594	19.2	594	US-10-029-386-25399	Sequence 25399, A
6	501	16.2	501	US-10-029-386-27556	Sequence 27556, A
7	411.2	13.3	449	US-09-918-995-27556	Sequence 27556, A
8	383.2	12.4	2416	US-10-032-233-19	Sequence 19, Appl1
9	383.2	12.4	2416	US-10-032-233-19	Sequence 19, Appl1
10	383.2	12.4	2416	US-10-032-233-19	Sequence 33, Appl1
11	383.2	12.4	2416	US-10-413-432-15	Sequence 15, Appl1

12	383.2	12.4	2416	18	US-10-413-432-19	Sequence 19, Appl1
13	383.2	12.4	2416	18 <td>US-10-413-432-33</td> <td>Sequence 33, Appl1</td>	US-10-413-432-33	Sequence 33, Appl1
14	383.2	12.4	2416	18 <td>US-10-324-466-15</td> <td>Sequence 15, Appl1</td>	US-10-324-466-15	Sequence 15, Appl1
15	383.2	12.4	2416	18 <td>US-10-324-466-19</td> <td>Sequence 19, Appl1</td>	US-10-324-466-19	Sequence 19, Appl1
16	383.2	12.4	2416	18 <td>US-10-324-466-33</td> <td>Sequence 33, Appl1</td>	US-10-324-466-33	Sequence 33, Appl1
17	381.6	12.3	1725	17 <td>US-10-326-892-1</td> <td>Sequence 1, Appl1</td>	US-10-326-892-1	Sequence 1, Appl1
18	381.6	12.3	1725	18 <td>US-10-326-892-1</td> <td>Sequence 1, Appl1</td>	US-10-326-892-1	Sequence 1, Appl1
19	381.6	12.3	1967	9 <td>US-09-748-739A-1</td> <td>Sequence 1, Appl1</td>	US-09-748-739A-1	Sequence 1, Appl1
20	381.6	12.3	2416	16 <td>US-10-032-233-11</td> <td>Sequence 3, Appl1</td>	US-10-032-233-11	Sequence 3, Appl1
21	381.6	12.3	2416	16 <td>US-10-032-233-11</td> <td>Sequence 11, Appl1</td>	US-10-032-233-11	Sequence 11, Appl1
22	381.6	12.3	2416	16 <td>US-10-032-233-17</td> <td>Sequence 17, Appl1</td>	US-10-032-233-17	Sequence 17, Appl1
23	381.6	12.3	2416	16 <td>US-10-032-233-27</td> <td>Sequence 27, Appl1</td>	US-10-032-233-27	Sequence 27, Appl1
24	381.6	12.3	2416	16 <td>US-10-032-233-35</td> <td>Sequence 35, Appl1</td>	US-10-032-233-35	Sequence 35, Appl1
25	381.6	12.3	2416	18 <td>US-10-413-432-11</td> <td>Sequence 11, Appl1</td>	US-10-413-432-11	Sequence 11, Appl1
26	381.6	12.3	2416	18 <td>US-10-413-432-17</td> <td>Sequence 17, Appl1</td>	US-10-413-432-17	Sequence 17, Appl1
27	381.6	12.3	2416	18 <td>US-10-413-432-27</td> <td>Sequence 27, Appl1</td>	US-10-413-432-27	Sequence 27, Appl1
28	381.6	12.3	2416	18 <td>US-10-413-432-35</td> <td>Sequence 35, Appl1</td>	US-10-413-432-35	Sequence 35, Appl1
29	381.6	12.3	2416	18 <td>US-10-324-466-11</td> <td>Sequence 11, Appl1</td>	US-10-324-466-11	Sequence 11, Appl1
30	381.6	12.3	2416	18 <td>US-10-324-466-17</td> <td>Sequence 17, Appl1</td>	US-10-324-466-17	Sequence 17, Appl1
31	381.6	12.3	2416	18 <td>US-10-324-466-27</td> <td>Sequence 27, Appl1</td>	US-10-324-466-27	Sequence 27, Appl1
32	381.6	12.3	2416	18 <td>US-10-324-466-35</td> <td>Sequence 35, Appl1</td>	US-10-324-466-35	Sequence 35, Appl1
33	380	12.3	2381	9 <td>US-09-880-107-2271</td> <td>Sequence 2271, Ap</td>	US-09-880-107-2271	Sequence 2271, Ap
34	380	12.3	2416	9 <td>US-09-748-739A-5</td> <td>Sequence 5, Appl1</td>	US-09-748-739A-5	Sequence 5, Appl1
35	380	12.3	2416	9 <td>US-09-748-739A-7</td> <td>Sequence 7, Appl1</td>	US-09-748-739A-7	Sequence 7, Appl1
36	380	12.3	2416	9 <td>US-09-748-739A-16</td> <td>Sequence 16, Appl1</td>	US-09-748-739A-16	Sequence 16, Appl1
37	380	12.3	2416	16 <td>US-10-032-233-13</td> <td>Sequence 13, Appl1</td>	US-10-032-233-13	Sequence 13, Appl1
38	380	12.3	2416	16 <td>US-10-032-233-29</td> <td>Sequence 29, Appl1</td>	US-10-032-233-29	Sequence 29, Appl1
39	380	12.3	2416	16 <td>US-10-032-233-31</td> <td>Sequence 31, Appl1</td>	US-10-032-233-31	Sequence 31, Appl1
40	380	12.3	2416	16 <td>US-10-032-233-37</td> <td>Sequence 37, Appl1</td>	US-10-032-233-37	Sequence 37, Appl1
41	380	12.3	2416	16 <td>US-10-032-233-39</td> <td>Sequence 39, Appl1</td>	US-10-032-233-39	Sequence 39, Appl1
42	380	12.3	2416	16 <td>US-10-032-233-43</td> <td>Sequence 43, Appl1</td>	US-10-032-233-43	Sequence 43, Appl1
43	380	12.3	2416	18 <td>US-10-413-432-13</td> <td>Sequence 13, Appl1</td>	US-10-413-432-13	Sequence 13, Appl1
44	380	12.3	2416	18 <td>US-10-413-432-29</td> <td>Sequence 29, Appl1</td>	US-10-413-432-29	Sequence 29, Appl1
45	380	12.3	2416	18 <td>US-10-413-432-31</td> <td>Sequence 31, Appl1</td>	US-10-413-432-31	Sequence 31, Appl1

## ALIGNMENTS

RESULT 1  
US-09-810-861B-5  
Sequence 5, Application US/09810861B  
Patent No. US20020162140A1

GENERAL INFORMATION:  
APPLICANT: Mori, Tsafir S.  
APPLICANT: Soreq, Hermona  
APPLICANT: Amlitz, Charles J.  
APPLICANT: Mason, Hugh S.

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN TRANSGENIC PLANTS

FILE REFERENCE: BTI-45

CURRENT APPLICATION NUMBER: US/09/810,861B

CURRENT FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/190,440

PRIOR FILING DATE: 2000-03-17

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patent In Ver. 3.1

SEQ ID NO 5

LENGTH: 1725

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURES:

OTHER INFORMATION: Description of Artificial Sequence: synthetic

OTHER INFORMATION: human acetylcholinesterase gene optimized for expression in plants

US-09-810-861B-5

Query Match 55.6%; Score 1722.4; DB 9; Length 1725;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1723; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
160 ATGAGGCCCCGAGTGTCTGTCGACACGCCCTTCGCTTCCGACATCTTCCTC 219

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using BW model

Run on: March 3, 2005, 06:55:38 ; Search time 500.214 Seconds  
(without alignments)  
10127.488 Million cell updates/sec

Title: US-09-310-638-3

Perfect score: 3096  
Sequence: 1 CCTCTCTCCCTCATCTTTG.....AAAAAAAAAAAAAAAAAAAA 3096

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

Issued Patents NA:  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PTCUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3096	100.0	3096	2	US-08-318-826A-6
2	3096	100.0	3096	2	US-08-370-156-3
3	3096	100.0	3096	2	US-08-814-095-3
4	2926	94.5	3016	2	US-08-318-826A-7
5	2926	94.5	3016	2	US-08-370-156-5
6	2926	94.5	3016	2	US-08-814-095-5
7	1888	61.0	2256	2	US-08-318-826A-5
8	1888	61.0	2256	2	US-08-370-156-1
9	1888	61.0	2256	2	US-08-814-095-1
10	1752.2	56.6	2158	4	US-09-949-016-1192
11	1752.2	56.6	2158	4	US-09-949-016-1193
12	1729	55.8	1845	4	US-07-732-962A-1
13	1729	55.8	1845	5	PCT-US92-06106-1
14	1722.4	55.6	1725	4	US-09-810-861B-5
15	1720	55.6	5767	4	US-09-810-861B-3
16	1720	55.6	14446	4	US-09-810-861B-4
17	1529.6	49.4	9885	4	US-09-949-016-12934
18	1529.6	49.4	9885	4	US-09-949-016-12935
19	1528	49.4	35060	3	US-08-814-095-7
20	1215	39.2	1215	2	US-08-370-156-26
21	380	12.3	2381	2	US-08-318-826A-9
22	380	12.3	2416	2	US-08-318-826A-8
23	380	12.3	2416	3	US-09-334-489-1
24	380	12.3	2416	3	US-09-334-489-2
25	380	12.3	2444	4	US-09-949-016-5275
26	378.4	12.2	2400	6	Patent No. 5215909
27	378.4	12.2	2400	6	Patent No. 5215909-13

28	374	12.1	374	2	US-08-370-156-24	Sequence 24, Appli
29	371.4	12.0	68667	4	US-09-949-016-17017	Sequence 17017, A
30	322.8	10.4	2445	6	5215909-9	Patent No. 5215909
31	322.8	10.4	2445	6	5215909-9	Patent No. 5215909
32	185.6	6.0	764	6	5215909-7	Patent No. 5215909
33	185.6	6.0	764	6	5215909-7	Patent No. 5215909
34	142.6	4.6	3018	1	US-08-347-718B-3	Sequence 3, Appli
35	142.6	4.6	3018	1	US-08-482-262-3	Sequence 3, Appli
36	141	4.6	2734	4	US-09-569-611C-5	Sequence 5, Appli
37	141	4.6	2781	4	US-09-569-611C-6	Sequence 6, Appli
38	141	4.6	3018	6	5200183-1	Patent No. 5200183
39	141	4.6	3018	6	5200183-1	Patent No. 5200183
40	139.4	4.5	1746	4	US-10-023-515-3	Sequence 3, Appli
41	139.4	4.5	2158	4	US-10-023-515-1	Sequence 1, Appli
42	139.4	4.5	2184	1	US-08-445-050-8	Sequence 8, Appli
43	139.4	4.5	2184	1	US-08-204-691-8	Sequence 8, Appli
44	139.4	4.5	2344	3	US-09-347-878-31	Sequence 31, Appli
45	139.4	4.5	2375	4	US-09-949-016-3976	Sequence 3976, Ap

#### ALIGNMENTS

RESULT 1  
US-08-318-826A-6  
Sequence 6, Application US/08318826A  
Patent No. 5891725  
GENERAL INFORMATION:  
APPLICANT: Soreq, Hermona  
APPLICANT: Zakut, Haim  
APPLICANT: Eckstein, Filtz  
TITLE OF INVENTION: Synthetic Antisense  
TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kohn & Associates  
STREET: 30500 No. 589175thweglein Hwy., Suite 410  
CITY: Farmington Hills  
STATE: Michigan  
COUNTRY: US  
ZIP: 48334  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/318,826A  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kohn, Kenneth I.  
REGISTRATION NUMBER: 30,955  
REFERENCE/DOCKET NUMBER: 2391.00001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (248) 539-5050  
TELEFAX: (248) 539-5055  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3096 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 160..1959  
OTHER INFORMATION: /note=Splice variant: Exons 1, 2,

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2005, 06:55:38 ; Search time 487,289 Seconds  
(without alignment)  
10127,488 Million cell updates/sec

Title: US-09-310-638-5  
Perfect score: 3016  
Sequence: 1 CCTCTCTCCCTCATCTTTG.....AAAAAAAAAAAAAAAAAAAA 3016

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 segs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3016	100.0	3016	2	US-08-318-826A-7
2	3016	100.0	3016	2	US-08-370-156-5
3	3016	100.0	3016	3	US-08-814-095-5
4	2926	97.0	3096	2	US-08-318-826A-6
5	2926	97.0	3096	2	US-08-370-156-3
6	2926	97.0	3096	2	US-08-814-095-3
7	1883.8	62.5	2256	2	US-08-318-826A-5
8	1883.8	62.5	2256	2	US-08-370-156-1
9	1883.8	62.5	2256	2	US-08-814-095-1
10	1748	58.0	2158	4	US-09-949-016-1192
11	1748	58.0	2158	4	US-09-949-016-1193
12	1724.8	57.2	1845	1	US-07-732-962A-1
13	1724.8	57.2	1845	5	PCT-US92-06106-1
14	1722	57.1	1725	4	US-09-810-861B-5
15	1720.2	57.0	1446	4	US-09-810-861B-3
16	1720.2	57.0	1446	4	US-09-810-861B-4
17	1359.6	45.1	9885	4	US-09-849-016-12934
18	1359.6	45.1	9885	4	US-09-849-016-12935
19	1358	45.0	35060	3	US-08-814-095-7
20	1135.8	37.7	1215	2	US-08-370-156-26
21	380	12.6	2381	2	US-08-318-826A-9
22	380	12.6	2416	2	US-08-318-826A-8
23	380	12.6	2416	3	US-09-334-489-1
24	380	12.6	2416	3	US-09-334-489-2
25	378.4	12.5	2400	4	US-09-949-016-5275
26	378.4	12.5	2400	6	US-09-949-016-5275
27	378.4	12.5	2400	6	US-09-949-016-5275

28	374	12.4	374	2	US-08-370-156-24	Sequence 24, Appl
29	371.4	12.3	6867	4	US-09-949-016-17017	Sequence 17017, A
30	322.8	10.7	2445	6	5215909-9	Patent No. 5215909
31	322.8	10.7	2445	6	5215909-9	Patent No. 5215909
32	185.6	6.2	764	6	5215909-7	Patent No. 5215909
33	185.6	6.2	764	6	5215909-7	Patent No. 5215909
34	144.2	4.8	3018	1	US-08-347-718B-3	Sequence 3, Appl1
35	144.2	4.8	3018	1	US-08-482-262-3	Sequence 3, Appl1
36	142.6	4.7	2734	4	US-09-589-611C-5	Sequence 5, Appl1
37	142.6	4.7	2781	4	US-09-589-611C-6	Sequence 6, Appl1
38	142.6	4.7	3018	6	5200183-1	Patent No. 5200183
39	142.6	4.7	3018	6	5200183-1	Patent No. 5200183
40	141	4.7	2184	1	US-08-445-050-8	Sequence 8, Appl1
41	141	4.7	2184	1	US-08-204-691-8	Sequence 31, Appl1
42	141	4.7	2344	3	US-09-347-878-31	Sequence 31, Appl1
43	141	4.7	2375	4	US-09-949-016-3976	Sequence 3976, Ap
44	141	4.7	2428	1	US-08-445-050-1	Sequence 1, Appl1
45	141	4.7	2428	1	US-08-204-691-1	Sequence 1, Appl1

## ALIGNMENTS

RESULT 1  
US-08-318-826A-7  
Sequence 7, Application US/08318826A  
Patent No. 5891725  
GENERAL INFORMATION:  
APPLICANT: Soreq, Hermona.  
APPLICANT: Zakut, Haim  
APPLICANT: Eckstein, Fritz  
TITLE OF INVENTION: Synthetic Antisense  
TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions  
TITLE OF INVENTION: Containing Them  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Kohn & Associates  
STREET: 30500 No. 5891725thwestern Hwy., Suite 410  
CITY: Farmington Hills  
STATE: Michigan  
COUNTRY: US  
ZIP: 48334  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/318,826A  
FILING DATE: 514  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kohn, Kenneth I.  
REGISTRATION NUMBER: 30,955  
REFERENCE/DOCKET NUMBER: 2391.00001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (248) 539-5050  
TELEFAX: (248) 539-5055  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3016 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 160..2010  
OTHER INFORMATION: /note= "Splice Variant: Exons 1, 2,

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

# OM nucleic - nucleic search, using sw model

Run on: March 3, 2005, 12:05:14 ; Search time 1640.27 Seconds

(without alignments)  
10910.664 Million cell updates/sec

Title: US-09-310-638-5

Perfect score: 3016  
Sequence: 1 CCTCTCTCCCTCATCTTTG.....AAAAAAAAAAAAAAAAAAAA 3016

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 5401638 seqs, 2966923429 residues

Total number of hits satisfying chosen parameters: 10803276

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

1:	/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2:	/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3:	/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6:	/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7:	/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8:	/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9:	/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10:	/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11:	/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12:	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13:	/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
14:	/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15:	/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16:	/cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17:	/cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18:	/cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19:	/cgn2_6/ptodata/1/pubpna/US10F_NEW_PUB.seq:*
20:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1722	57.1	1725	US-09-810-861B-5	Sequence 5, Appl1
2	1720.2	57.0	5767	US-09-810-861B-3	Sequence 3, Appl1
3	1720.2	57.0	14446	US-09-810-861B-4	Sequence 4, Appl1
C	740	24.5	740	US-10-029-386-22811	Sequence 22811, A
C	594	19.7	594	US-10-029-386-25399	Sequence 25399, A
C	5	501	16.6	US-10-029-386-21596	Sequence 21596, A
7	411.2	13.6	449	US-09-918-995-27556	Sequence 27556, A
8	383.2	12.7	2416	US-10-032-233-15	Sequence 15, Appl1
9	383.2	12.7	2416	US-10-032-233-19	Sequence 19, Appl1
10	383.2	12.7	2416	US-10-032-233-33	Sequence 33, Appl1
11	383.2	12.7	2416	US-10-413-432-31	Sequence 31, Appl1

12	383.2	12.7	2416	US-10-413-432-19	Sequence 19, Appl1
13	383.2	12.7	2416	US-10-413-432-33	Sequence 33, Appl1
14	383.2	12.7	2416	US-10-324-466-15	Sequence 15, Appl1
15	383.2	12.7	2416	US-10-324-466-19	Sequence 19, Appl1
16	383.2	12.7	2416	US-10-324-466-33	Sequence 33, Appl1
17	383.2	12.7	1725	US-10-326-892-1	Sequence 1, Appl1
18	381.6	12.7	1725	US-10-326-892-1	Sequence 1, Appl1
19	381.6	12.7	1967	US-09-748-739A-1	Sequence 1, Appl1
20	381.6	12.7	2416	US-09-748-739A-3	Sequence 3, Appl1
21	381.6	12.7	2416	US-10-032-233-11	Sequence 11, Appl1
22	381.6	12.7	2416	US-10-032-233-17	Sequence 17, Appl1
23	381.6	12.7	2416	US-10-032-233-27	Sequence 27, Appl1
24	381.6	12.7	2416	US-10-032-233-35	Sequence 35, Appl1
25	381.6	12.7	2416	US-10-413-432-11	Sequence 11, Appl1
26	381.6	12.7	2416	US-10-413-432-17	Sequence 17, Appl1
27	381.6	12.7	2416	US-10-413-432-27	Sequence 27, Appl1
28	381.6	12.7	2416	US-10-413-432-35	Sequence 35, Appl1
29	381.6	12.7	2416	US-10-324-466-11	Sequence 11, Appl1
30	381.6	12.7	2416	US-10-324-466-17	Sequence 17, Appl1
31	381.6	12.7	2416	US-10-324-466-27	Sequence 27, Appl1
32	381.6	12.7	2416	US-10-324-466-35	Sequence 35, Appl1
33	380	12.6	2381	US-09-880-107-2271	Sequence 2271, Ap
34	380	12.6	2416	US-09-748-739A-5	Sequence 5, Appl1
35	380	12.6	2416	US-09-748-739A-7	Sequence 7, Appl1
36	380	12.6	2416	US-09-748-739A-16	Sequence 16, Appl1
37	380	12.6	2416	US-10-032-233-13	Sequence 13, Appl1
38	380	12.6	2416	US-10-032-233-29	Sequence 29, Appl1
39	380	12.6	2416	US-10-032-233-31	Sequence 31, Appl1
40	380	12.6	2416	US-10-032-233-37	Sequence 37, Appl1
41	380	12.6	2416	US-10-032-233-39	Sequence 39, Appl1
42	380	12.6	2416	US-10-032-233-43	Sequence 43, Appl1
43	380	12.6	2416	US-10-413-432-13	Sequence 13, Appl1
44	380	12.6	2416	US-10-413-432-29	Sequence 29, Appl1
45	380	12.6	2416	US-10-413-432-31	Sequence 31, Appl1

## ALIGNMENTS

RESULT 1  
US-09-810-861B-5  
Sequence 5, Application US/09810861B  
Patent No. US20020162140A1  
GENERAL INFORMATION:  
APPLICANT: Mor, Teafir S.  
APPLICANT: Soreq, Hermona  
APPLICANT: Amltzen, Charles J.  
APPLICANT: Mason, Hugh S.  
TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN TRANSGENIC PLANTS  
FILE REFERENCE: BTI-45  
CURRENT APPLICATION NUMBER: US/09/810, 861B  
CURRENT FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/190,440  
PRIOR FILING DATE: 2000-03-17  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn Ver. 3.1  
SEQ ID NO 5  
LENGTH: 1725  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
OTHER INFORMATION: human acetylcholinesterase gene optimized for expression in plants  
US-09-810-861B-5

Query Match 57.1%; Score 1722; DB 9; Length 1725;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
160 ATGAGCGCCCGGCGATGCTGCTGACACGCGCTTCCGCTTCCGCTTCTCTC 219  
|||||